



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: THE ROCKEFELLER UNIVERSITY
- (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
- (iii) NUMBER OF SEQUENCES: 100
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Klauber & Jackson
 - (B) STREET: 411 Hackensack Avenue
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/485,943
 - (B) FILING DATE: June 7, 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/438,431
 - (B) FILING DATE: May 10, 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/347,563
 - (B) FILING DATE: November 30, 1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/292,345
 - (B) FILING DATE: August 17, 1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
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 - (A) TELEPHONE: 201 487-5800
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 - (C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2793 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
 - (A) DESCRIPTION: Murine ob cDNA
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCCCTGC	TCCAGCAGCT	GCAAGGTGCA	AGAAGAAGAA	GATCCCAGGG	AGGAAA	56
ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG	104					
Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu						
1 5 10 15						
TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA	152					
Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys						
20 25 30						
ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG	200					
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr						
35 40 45						
CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT	248					
Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro						
50 55 60						
GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA	296					
Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala						
65 70 75 80						
GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG	344					
Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln						
85 90 95						
ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC	392					
Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala						
100 105 110						
TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA	440					
Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro						
115 120 125						
GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG	488					
Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val						
130 135 140						
GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG	536					
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln						
145 150 155 160						
TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA	588					
Leu Asp Val Ser Pro Glu Cys *						
165						
ATCATGTAGA GGGAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC	648					
ACACATCCAT CATTCAATTC TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA	708					
CAATGCTTGA CTCAAGTTAT CCACACAAC TCAATGAGCAC AAGGAGGGGC CAGCCTGCAG	768					
AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG	828					
TCCCACCTGC TCCGGGTACA TGTTCTCCCG TGGGTACACG CTTGCTGCG GCCCAGGAGA	888					
GGTGAGGTAG GGATGGGTAG AGCCTTTGGG CTGTCTCAGA GTCTTTGGGA GCACCGTGAA	948					

GGCTGCATCC	ACACACAGCT	GGAAACTCCC	AAGCAGCACA	CGATGGAAGC	ACTTATTTAT	1008
TTATTCTGCA	TTCTATTTTG	GATGGATCTG	AAGCAAGGCA	TCAGCTTTTT	CAGGCTTTGG	1068
GGGTCAGCCA	GGATGAGGAA	GGCTCCTGGG	GTGCTGCTTT	CAATCCTATT	GATGGGTCTG	1128
CCCAGGGCAA	ACCTAATTTT	TGAGTGACTG	GAAGGAAGGT	TGGGATCTTC	CAAACAAGAG	1188
TCTATGCAGG	TAGCGCTCAA	GATTGACCTC	TGGTGACTGG	TTTTGTTTCT	ATTGTGACTG	1248
ACTCTATCCA	AACACGTTTG	CAGCGGCATT	GCCGGGAGCA	TAGGCTAGGT	TATTATCAAA	1308
AGCAGATGAA	TTTTGTCAAG	TGTAATATGT	ATCTATGTGC	ACCTGAGGGT	AGAGGATGTG	1368
TTAGAGGGAG	GGTGAAGGAT	CCGGAAGTGT	TCTCTGAATT	ACATATGTGT	GGTAGGCTTT	1428
TCTGAAAGGG	TGAGGCATTT	TCTTACCTCT	GTGGCCACAT	AGTGTGGCTT	TGTGAAAAGG	1488
ACAAAGGAGT	TGACTCTTTC	CGGAACATTT	GGAGTGTACC	AGGCACCCTT	GGAGGGGCTA	1548
AAGCTACAGG	CCTTTTGTTG	GCATATTGCT	GAGCTCAGGG	AGTGAGGGCC	CCACATTTGA	1608
GACAGTGAGC	CCCAAGAAAA	GGGTCCCTGG	TGTAGATCTC	CAAGGTTGTC	CAGGGTTGAT	1668
CTCACAATGC	GTTTCTTAAG	CAGGTAGACG	TTTGCATGCC	AATATGTGGT	TCTCATCTGA	1728
TTGGTTTCATC	CAAAGTAGAA	CCCTGTCTCC	CACCCATTCT	GTGGGGAGTT	TTGTTCCAGT	1788
GGGAATGAGA	AATCACTTAG	CAGATGGTCC	TGAGCCCTGG	GCCAGCACTG	CTGAGGAAGT	1848
GCCAGGGCCC	CAGGCCAGGC	TGCCAGAATT	GCCCTTCGGG	CTGGAGGATG	AACAAAGGGG	1908
CTTGGGTTTT	TCCATCACCC	CTGCACCCTA	TGTCACCATC	AAACTGGGGG	GCAGATCAGT	1968
GAGAGGACAC	TTGATGGAAA	GCAATACACT	TTAAGACTGA	GCACAGTTTC	GTGCTCAGCT	2028
CTGTCTGGTG	CTGTGAGCTA	GAGAAGCTCA	CCACATACAT	ATAAAAAATCA	GAGGCTCATG	2088
TCCCTGTGGT	TAGACCCCTAC	TCGCGGCGGT	GTA CTCCACC	ACAGCAGCAC	CGCACCCTG	2148
GAAGTACAGT	GCTGTCTTCA	ACAGGTGTGA	AAGAACCTGA	GCTGAGGGTG	ACAGTGCCCA	2208
GGGGAACCCCT	GCTTGCAGTC	TATTGCATTT	ACATACCGCA	TTTCAGGGCA	CATTAGCATC	2268
CACTCCTATG	GTAGCACACT	GTTGACAATA	GGACAAGGGA	TAGGGGTTGA	CTATCCCTTA	2328
TCCAAAATGC	TTGGGACTAG	AAGAGTTTTG	GATTTTAGAG	TCTTTTCAGG	CATAGGTATA	2388
TTTGAGTATA	TATAAAATGA	GATATCTTGG	GGATGGGGCC	CAAGTATAAA	CATGAAGTTC	2448
ATTTATATTT	CATAATACCG	TATAGACACT	GCTTGAAGTG	TAGTTTTATA	CAGTGTTTTA	2508
AATAACGTTG	TATGCATGAA	AGACGTTTTT	ACAGCATGAA	CCTGTCTACT	CATGCCAGCA	2568
CTCAAAAACC	TTGGGGTTTT	GGAGCAGTTT	GGATCTTGGG	TTTTCTGTTA	AGAGATGGTT	2628
AGCTTATACC	TAAAACCATA	ATGGCAAACA	GGCTGCAGGA	CCAGACTGGA	TCCTCAGCCC	2688
TGAAGTGTGC	CCTTCAGCC	AGGTCATACC	CTGTGGAGGT	GAGCGGGATC	AGGTTTTGTG	2748
GTGCTAAGAG	AGGAGTTGGA	GGTAGATTTT	GGAGGATCTG	AGGGC		2793

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: Murine ob polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
 1           5           10           15
Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
          20           25           30
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
          35           40           45
Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
          50           55           60
Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
 65           70           75           80
Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
          85           90           95
Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
          100          105          110
Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
          115          120          125
Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
          130          135          140
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
          145          150          155          160
Leu Asp Val Ser Pro Glu Cys
          165
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) DESCRIPTION: Human ob cDNA where N represents any nucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 46..546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
NNNGNNGTTG CAAGGCCCAA GAAGCCCAANN NTCCTGGGAA GGAAA ATG CAT TGG
                                     Met His Trp
                                     1
```

GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val 5 10 15	102
CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile 20 25 30 35	150
AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val 40 45 50	198
TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His 55 60 65	246
CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln 70 75 80	294
CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn 85 90 95	342
GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys 100 105 110 115	390
AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC CTG Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu 120 125 130	438
GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC CTG Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu 135 140 145	486
AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu 150 155 160	534
AGC CCT GGG TGC TGAGGCCTT GAAGGTCACT CTCCTGCAA GGACTNACGT Ser Pro Gly Cys 165	585
TAAGGGAAGG AACTCTGGTT TCCAGGTATC TCCAGGATTG AAGAGCATTG CATGGACACC	645
CCTTATCCAG GACTCTGTCA ATTTCCCTGA CTCCTCTAAG CCACTCTTCC AAAGG	700

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Human ob polypeptide

(vi) ORIGINAL SOURCE: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu 1 5 10 15
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys 20 25 30

Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
 50 55 60
 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
 65 70 75 80
 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
 85 90 95
 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
 100 105 110
 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
 115 120 125
 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
 130 135 140
 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
 145 150 155 160
 Leu Asp Leu Ser Pro Gly Cys
 165

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide lacking Gln at position

49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
 1 5 10 15
 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
 Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly
 50 55 60
 Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val
 65 70 75 80
 Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile
 85 90 95
 Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe
 100 105 110

Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu
115 120 125

Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
130 135 140

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu
145 150 155 160

Asp Val Ser Pro Glu Cys
165

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) Description: Human ob polypeptide lacking Gln at position

49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
1 5 10 15

Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30

Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45

Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly
50 55 60

Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val
65 70 75 80

Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile
85 90 95

Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe
100 105 110

Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp
115 120 125

Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val
130 135 140

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu
145 150 155 160

Asp Leu Ser Pro Gly Cys
165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(A) DESCRIPTION: exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG TGTCGGGTCC	60
NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC TATCCAGAAA GTCCAGGATG	120
ACACCAAAAG CCTCATCAAG ACCATTGTCA NCAGGATCAC TGANATTTCA CACACG	176

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: PCR 5' primer for exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCAGGGCAGG AAAATGTG	18
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: PCR 3' primer for exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATCCTGGAC TTTCTGGATA GG	22
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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: putative N-terminal signal peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
1      5      10      15
Ser Tyr Val Gln Ala Val Pro
20
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (plasmid)

(A) DESCRIPTION: pET-15b expression vector

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: T7 promoter
(B) LOCATION: 20..37

(ix) FEATURE:

(A) NAME/KEY: lac operator
(B) LOCATION: 39..64

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 108..243

(ix) FEATURE:

(A) NAME/KEY: His-Tag
(B) LOCATION: 123..137

(ix) FEATURE:

(A) NAME/KEY: Thrombin cleavage site
(B) LOCATION: 184..196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA      60
TTCCCCTCTA CAAATAATTT TGTTTAACTT TAAGAAGGAG ATATACC ATG GGC AGC      116
                                     Met Gly Ser
                                     1
AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG CGC GGC AGC      164
Ser His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
5      10      15
CAT ATG CTC GAG GAT CCC GCT GCT AAC AAA GCC CGA AAG GAA GCT GAG      212
His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys Glu Ala Glu
20     25     30     35
TTG GCT GCT GCC ACC GCT GAG CAA TAA CTA G CATAACCCCT TGGGGCCTCT      263
Leu Ala Ala Ala Thr Ala Glu Gln *
40
AAACGGGTCT TGAGGGGTTT TTTG      287
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15
Arg Gly Ser His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys
20 25 30
Glu Ala Glu Leu Ala Ala Ala Thr Ala Glu Gln
35 40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Murine 5' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTATGTTCA TATGGTGCCG ATCCAGAAAG TC
32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Murine 3' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCCCTCTACA TATGTCTTGG GAGCCTGGTG GC
32

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Human 5' primer
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTATGTCCA TATGGTGCCG ATCCAAAAAG TC
32

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Human 3' primer
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: Yes
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCCTTCCCA TATGGTACTC CTTGCAGGAA GA
32

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - (A) DESCRIPTION: Splice acceptor site in ob
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: Splice acceptor site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCAGTCGGT A

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
 - (A) DESCRIPTION: ob peptide fragment
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr	Leu	Ile	Lys	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
 - (A) DESCRIPTION: ob peptide fragment
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu	His	Pro	Ile	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
 - (A) DESCRIPTION: ob peptide fragment
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser	Lys	Ser	Cys	Ser	Leu	Pro	Gln	Thr	Ser	Gly	Leu	Gln	Lys	Pro	Glu
1				5				10						15	

Ser Leu Asp

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
 (A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: Carboxyl terminal

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Ile	Leu	Gln	Gln	Leu	Asp	Val
1				5					10					15	
Ser	Pro	Glu	Cys												
			20												

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
 (A) DESCRIPTION: portion of the human ob gene including noncoding sequence upstream of first exon, coding sequence of first exon, and 5' region of first intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 38..181

(ix) FEATURE:
 (A) NAME/KEY: 5' region of first intron
 (B) LOCATION: 182..414

(ix) FEATURE:
 (A) NAME/KEY: 5' noncoding sequence of the human ob gene from which the HOB lgF DNA primer was generated
 (B) LOCATION: 11..28

(ix) FEATURE:
 (A) NAME/KEY: intronic sequence of the human ob gene from which the HOB lgR primer was generated
 (B) LOCATION: 241..260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTTGCAAGG	CCCAAGAAGC	CCATCCTGGG	AAGGAAA	ATG	CAT	TGG	GGA	ACC	CTG		55					
				Met	His	Trp	Gly	Thr	Leu							
				1				5								
TGC	GGA	TTC	TTG	TGG	CTT	TGG	CCC	TAT	CTT	TTC	TAT	GTC	CAA	GCT	GTG	103
Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	Leu	Phe	Tyr	Val	Gln	Ala	Val	
			10					15					20			

CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC AAG ACA ATT	151
Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile	
25 30 35	
GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG GTAAGGAGAG TATGCGGGGA	201
Val Thr Arg Ile Asn Asp Ile Ser His Thr	
40 45	
CAAAGTAGAA CTGCAGCCAG CCCAGCACTG GCTCCTAGTG GCACTGGACC CAGATAGTCC	261
AAGAAACATT TATTGAACGC CTCCTGAATG CCAGGCACCT ACTGGAAGCT GAGAAGGATT	321
TTGGATAGCA CAGGGCTCCA CTCTTTCTGG TTGTTTCTTN TGGCCCCCTC TGCCTGCTGA	381
GATNCCAGGG GTTAGNGGTT CTTAATTCCT AAA	414

(ix) FEATURE:
 (A) NAME/KEY: intronic sequence of the human ob gene HOB from
 which the HOB 2gF primer was generated
 (B) LOCATION: 250..269

(ix) FEATURE:
 (A) NAME/KEY: 3' noncoding sequence of the human ob gene from
 which the HOB 2gR DNA primer was generated
 (B) LOCATION: 707..728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGGTTCTTT CAGGAAGAGG CCATGTAAGA GAAAGGAATT GACCTAGGGA AAATTGGCCT	60
GGGAAGTGGG GGAACGGAT GGTGTGGGAA AAGCAGGAAT CTCGGAGACC AGCTTAGAGG	120
CTTGGCAGTC ACCTGGGTGC AGGANACAAG GGCCTGAGCC AAAGTGGTGA GGGAGGGTGG	180
AAGGAGACAG CCCAGAGAAT GACCCTCCAT GCCCACGGGG AAGGCAGAGG GCTCTGAGAG	240
CGATTCTCC CACATGCTGA GCACTTGTTT TCCCTCTTCC TCCTNCATAG CAG TCA	296
	Gln Ser
	1
GTC TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC	344
Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu	
	5 10 15
CAC CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC	392
His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr	
	20 25 30
CAA CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC	440
Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser	
	35 40 45 50
AAC GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT	488
Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser	
	55 60 65
AAG AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC	536
Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser	
	70 75 80
CTG GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC	584
Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala	
	85 90 95
CTG AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC	632
Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp	
	100 105 110
CTC AGC CCT GGG TGC T GAGGCCTTGA AGGTCACTCT TCCTGCAAGG ACTACGTTAA	688
Leu Ser Pro Gly Cys	
	115
GGGAAGGAAC TCTGGCTTTC CAGGTATCTC CAGGATTGAA GAGCATTGCA TGGACACCCC	748
TTATCCAGGA CTCTGTCAAT TTCCCTGACT CCTCTAAGCC ACTCTTCCAA AGG	801

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: C-terminal portion of the human ob protein
encoded by second exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
1 5 10 15
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
20 25 30
Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
35 40 45
Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
50 55 60
Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
65 70 75 80
Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
85 90 95
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
100 105 110
Leu Asp Leu Ser Pro Gly Cys
115

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Glu Lys Arg Glu Ala Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu Ala Glu Ala
1

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: Internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Glu Lys Arg
1

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: HOB lgF DNA primer generated from the 5' noncoding sequence of the human ob gene
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCAAGAAGC CCATCCTG

18

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: HOB lgR DNA primer generated from the first intronic sequence of the human ob gene
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTATCTGG GTCCAGTGCC

20

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: HOB 2gF DNA primer generated from the first
intronic sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCACATGCTG AGCACTTGTT

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: HOB 2gR DNA primer generated from the 3'
noncoding sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTCAATCCT GGAGATACCT GG
22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA
(A) DESCRIPTION: pPIC.9 cloning site

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCGAGAAAA GAGAGGCTGA AGCTTACGTA GAATTCCCTA GGCCGGCCGG G

51

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 5' primer for amplifying human ob cDNA
sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTATCTCTCG AGAAAAGAGT GCCCATCCAA AAAGTCCAAG
40

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 3' primer for amplifying human ob cDNA
sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCGCGAATTC TCAGCACCCA GGGCTGAGGT C
31

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 5' primer for amplifying murine ob cDNA
sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTATCTCTCG AGAAAAGAGT GCCTATCCAG AAAGTCCAGG
40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 3' primer for amplifying murine ob cDNA
sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCGAATTC TCAGCATTCA GGGCTAACAT C

31

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: tetrapeptide at N-terminus of renatured
murine ob protein after thrombin cleavage

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Ser His Met

1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1734

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGACAAAT GAGATAAGG

19

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1734

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAGTTACAG CTTTACAG

18

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS494
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTAAACACCT TTCCATTCC

19

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS494
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TTATATTCAC TTTCCCCTC TC
22

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer swSS883

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGCAGTAAGC TGTGATTGAG

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS883

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTGCAGCTTT AATTGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2359

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AGTGTGTGTG TTCTCCTG

18

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2359

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAAGGGGATG TGATAAGTG

19

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2336

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTGTTACGT TTAGTTAC

18

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2336

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGAATAATGA GAGAAGATTG

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1218

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTCAACTGA CAGAAAAC

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1218

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GACTATGTAA AAGAAATGCC

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1402

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AAAGGGCTTC TAATCTAC

18

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
 (A) DESCRIPTION: sequence tagged-site specific PCR primer
 sWSS1402

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
 CCTTCCAAC TCTTTGAC 18

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
 (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS999

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
 TAAACCCCT TTCTGTTC 18

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
 (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS999

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
 TTGCATAATA GTCACACCC 19

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1751

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCAAAATCAG AATTGTCAGA AG 22

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1751

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAACCGAAGT TCAGATACAG 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1174

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AATATCTGAC ATTGGCAC 18

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1174

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TTAGACCTGA GAAAAGAG 18

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2061

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GTTGCACAAT ACAAATCC 19

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2061

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTTCCATTAG TGTCTTATAG 20

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCACTACAC ACCTAATC

18

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCATTCTACA TTTCCACC

18

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS808
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GGCTGTGTGA GCAAGATCCT AGGA

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS808
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TTGCCAGGCA AAGAGGGCTG GAC

23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1392
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTCAGGTATG TCTTTATC

18

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1392
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGTCTCTGCA TTCTTTTC

18

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer
- sWSS1148
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GACACATACA AACACAAG

18

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer
- sWSS1148
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
ATTGAGTTGA GTGTAGTAG

19

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer
- sWSS1529
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGGATTTC TAATTGTC

18

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS1529

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AAAAGATGGA GGCTTTTG

18

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2619

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGTTAAGGGA AGGAACTCTG G

21

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2619

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGCTTAGAG GAGTCAGGGA

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS404

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCAGGGTCA ATACAAAG

18

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS404

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TAATGTGTCC TTCTTGCC

18

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: sequence tagged-site specific PCR primer
sWSS2367

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAATCCTGGC TTCATTTG

18

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer
- sWSS2367
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGGTGGGTA GGATGCTA

18

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Marker UT528
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGCAGTAAGC TGTGATTGAG

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Marker UT528
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTGCAGCTTT AATTGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFMa065zg9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGCTTCAAGA CTTNAGCCT

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFMa065zg9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGTCAGCAGC ACTGTGATT

19

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFMa125wh1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
TCACCTTGAG ATTCCATCC 19

(2) INFORMATION FOR SEQ ID NO:82:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (primer)
 (A) DESCRIPTION: Marker AFMa125wh1
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
AACACCGTGG TCTTATCAAA 20

(2) INFORMATION FOR SEQ ID NO:83:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (primer)
 (A) DESCRIPTION: Marker AFM309yf10
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
CATCCAAGTT GGCAGTTTTT 20

(2) INFORMATION FOR SEQ ID NO:84:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (primer)
 (A) DESCRIPTION: Marker AFM309yf10
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AGATGCTGAA TTCCAGACA

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFM218xf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGGGCAACAC AGCAAA

16

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFM218xf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCAGTTAGT GCCAATGTCA

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFM206xc1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCAGGCCATG TGGAAC

16

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFM206xc1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGTTCTTGGC TTGCGTCAGT

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFM199xh12

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCTGATTGCT GGCTGC

16

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFM199xh12

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCGCGTGTGT ATGTGAG

17

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFMa345wc9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTCTTGGC AAATCACAT

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFMa345wc9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCCTAAGGGA ATGAGACACA

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: primer for mouse Pax4 gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGAGCCTTG TCCTGGGTAC AAAG

24

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(A) DESCRIPTION: Recombinant murine met ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: murine

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 41..478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TCTAGATTTG AGTTTAACT TTTAGAAGGA GGAATAACAT ATG GTA CCG ATC CAG	55
Met Val Pro Ile Gln	
1 5	
AAA GTT CAG GAC GAC ACC AAA ACC TTA ATT AAA ACG ATC GTT ACG CGT	103
Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg	
10 15 20	
ATC AAC GAC ATC AGT CAC ACC CAG TCG GTC TCC GCT AAA CAG CGT GTT	151
Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ala Lys Gln Arg Val	
25 30 35	
ACC GGT CTG GAC TTC ATC CCG GGT CTG CAC CCG ATC CTA AGC TTG TCC	199
Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser	
40 45 50	
AAA ATG GAC CAG ACC CTG GCT GTA TAC CAG CAG GTG TTA ACC TCC CTG	247
Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu	
55 60 65	
CCG TCC CAG AAC GTT CTT CAG ATC GCT AAC GAC CTC GAG AAC CTT CGC	295
Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg	
70 75 80 85	
GAC CTG CTG CAC CTG CTG GCA TTC TCC AAA TCC TGC TCC CTG CCG CAG	343
Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln	
90 95 100	
ACC TCA GGT CTT CAG AAA CCG GAA TCC CTG GAC GGG GTC CTG GAA GCA	391
Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu Ala	
105 110 115	
TCC CTG TAC AGC ACC GAA GTT GTT GCT CTG TCC CGT CTG CAG GGT TCC	439
Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser	

120	125	130	
CTT CAG GAC ATC CTT CAG CAG CTG GAC GTT TCT CCG GAA TGT TAATGGA			488
Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu Cys			
135	140	145	
TCC			491

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Recombinant murine met ob protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr	Leu	Ile	Lys
1				5					10					15	
Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	Gln	Ser	Val	Ser
			20				25						30		
Ala	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	Gly	Leu	His	Pro
		35					40					45			
Ile	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	Val	Tyr	Gln	Gln
	50					55					60				
Val	Leu	Thr	Ser	Leu	Pro	Ser	Gln	Asn	Val	Leu	Gln	Ile	Ala	Asn	Asp
65					70					75				80	
Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Leu	Leu	Ala	Phe	Ser	Lys	Ser
				85				90						95	
Cys	Ser	Leu	Pro	Gln	Thr	Ser	Gly	Leu	Gln	Lys	Pro	Glu	Ser	Leu	Asp
			100					105					110		
Gly	Val	Leu	Glu	Ala	Ser	Leu	Tyr	Ser	Thr	Glu	Val	Val	Ala	Leu	Ser
		115					120					125			
Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Ile	Leu	Gln	Gln	Leu	Asp	Val	Ser
	130					135					140				
Pro	Glu	Cys													
145															

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (A) DESCRIPTION: Recombinant human met ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 4..444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAT	ATG	GTA	CCG	ATC	CAG	AAA	GTT	CAG	GAC	GAC	ACC	AAA	ACC	TTA	ATT	48
Met	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr	Leu	Ile		
1				5				10					15			
AAA	ACG	ATC	GTT	ACG	CGT	ATC	AAC	GAC	ATC	AGT	CAC	ACC	CAG	TCG	GTG	96
Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	Gln	Ser	Val	
				20				25					30			
AGC	TCT	AAA	CAG	CGT	GTT	ACA	GGC	CTG	GAC	TTC	ATC	CCG	GGT	CTG	CAC	144
Ser	Ser	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	Gly	Leu	His	
			35					40					45			
CCG	ATC	CTG	ACC	TTG	TCC	AAA	ATG	GAC	CAG	ACC	CTG	GCT	GTA	TAC	CAG	192
Pro	Ile	Leu	Thr	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	Val	Tyr	Gln	
		50					55					60				
CAG	ATC	TTA	ACC	TCC	ATG	CCG	TCC	CGT	AAC	GTT	CTT	CAG	ATC	TCT	AAC	240
Gln	Ile	Leu	Thr	Ser	Met	Pro	Ser	Arg	Asn	Val	Leu	Gln	Ile	Ser	Asn	
	65					70				75						
GAC	CTC	GAG	AAC	CTT	CGC	GAC	CTG	CTG	CAC	GTG	CTG	GCA	TTC	TCC	AAA	288
Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala	Phe	Ser	Lys	
80					85				90						95	
TCC	TGC	CAC	CTG	CCA	TGG	GCT	TCA	GGT	CTT	GAG	ACT	CTG	GAC	TCT	CTG	336
Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu	Asp	Ser	Leu	
				100				105						110		
GGC	GGG	GTC	CTG	GAA	GCA	TCC	GGT	TAC	AGC	ACC	GAA	GTT	GTT	GCT	CTG	384
Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val	Val	Ala	Leu	
		115					120					125				
TCC	CGT	CTG	CAG	GGT	TCC	CTT	CAG	GAC	ATG	CTT	TGG	CAG	CTG	GAC	CTG	432
Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln	Leu	Asp	Leu	
		130				135						140				
TCT	CCG	GGT	TGT	TAATGGATCC												454
Ser	Pro	Gly	Cys													
	145															

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: Recombinant human met ob protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr	Leu	Ile	Lys
1				5				10					15		
Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	Gln	Ser	Val	Ser
		20				25						30			
Ser	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	Gly	Leu	His	Pro
		35				40						45			

Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
 50 55 60
 Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
 65 70 75 80
 Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
 85 90 95
 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
 100 105 110
 Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
 115 120 125
 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
 130 135 140
 Pro Gly Cys
 145

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met
 20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser Pro
 20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(A) DESCRIPTION: tripeptide at N-terminus of
ob protein after thrombin cleavage

(vi) ORIGINAL SOURCE:
(A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Gly Ser Pro